

Genetic profile for Eagle Creek NFH
coho salmon

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Prepared by

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National Fish Hatchery Broodstock Genetic Profile

Facility: Eagle Creek National Fish Hatchery

Stock: coho salmon (*Oncorhynchus kisutch*)

Parental stock: The broodstock at Eagle Creek NFH was originally developed in the late 1950s from early-run (Type S) Sandy River, Toutle River, Big Creek, and Elochoman River stocks, all of which are outside the Clackamas River watershed but within the Lower Columbia River Coho Evolutionarily Significant Unit (ESU) ^{Ref 1}.

Year founded: 1956

Generation time: 2 years (1.4%) to 3 years (98.6%) ^{Ref 2}.

Segregation / Integration history: Segregated.

Table 1 – Hatchery samples analyzed:

Description	H/ W	Run type	Collection year	Brood year	n	Life stage	Data source
Eagle Creek NFHa	H	Early	2001	1998	93	returning adult	NOAA
Eagle Creek NFHa	H	Early	2010	2007	117	returning adult	AFTC
Eagle Creek NFHa	H	Early	2011	2008	148	returning adult	AFTC
Eagle Creek NFHj	H	Early	2010	2009	99	juvenile	AFTC
Eagle Creek NFHj	H	Early	2012	2010	100	juvenile	AFTC

Table 2 – Coho salmon samples analyzed for comparison:

Description	H/W	Run type	Collection year	Brood year	n	Life stage	Data source
Big	H	Early	2002	2001	66	juvenile	NOAA
Bonneville	H	Early	2002	2001	74	juvenile	NOAA
Clackamas	W	Early	1998	1995	28	returning adult	NOAA
Clackamas	W	Early	2010	2007	96	returning adult	AFTC
Clackamas	W	Early	2011	2008	89	returning adult	AFTC
Clackamas	W	Late	1998	1995	27	returning adult	NOAA
Clackamas	W	Late	2010	2007	78	returning adult	AFTC
Clackamas	W	Late	2011	2008	66	returning adult	AFTC
Clear	W	Early	2007	2005	39	juvenile	AFTC
Clear	W	Early	2008	2006	45	juvenile	AFTC
Clear	W	Early	2010	2009	97	Juvenile	AFTC
Clear	W	Early	2011	2010	33	Juvenile	AFTC
Cowlitz	H	Late	2002	2001	77	juvenile	NOAA
Cowlitz	H	Late	2003	2002	45	juvenile	NOAA
Deep	W	Early	2007	2005	43	juvenile	AFTC
Deep	W	Early	2008	2006	58	juvenile	AFTC
Eagle	W	Early	2008	2006	56	juvenile	AFTC
Eagle	W	Early	2010	2009	96	Juvenile	AFTC
Eagle	W	Early	2011	2010	74	Juvenile	AFTC
Elochoman	H	Early	2003	2002	43	juvenile	NOAA
Elochoman	H	Late	2003	2002	42	juvenile	NOAA
Fallert	H	Early	2003	2001	47	juvenile	NOAA
Fallert	H	Early	2003	2002	42	juvenile	NOAA
Kalama	H	Late	2003	2001	35	juvenile	NOAA
Kalama	H	Late	2003	2002	29	juvenile	NOAA
Lewis	H	Early	2003	2002	35	juvenile	NOAA
Lewis	H	Late	2003	2002	46	juvenile	NOAA
North Fork Eagle	W	Early	2010	2009	88	Juvenile	AFTC
North Fork Eagle	W	Early	2011	2010	83	Juvenile	AFTC
Sandy	H	Early	2002	2001	84	juvenile	NOAA
Toutle	H	Early	2002	1999	80	returning adult	AFTC

Genetic markers analyzed:

11 microsatellites standardized between NOAA Fisheries Manchester Field Station and AFTC ^{Ref}
³ (11 / 11 loci). A complete list of the markers analyzed is provided in Appendix 1. Genotyping success rates are presented in Appendix 2.

Table 3 - Diversity within samples. Expected (H_e) and observed (H_o) heterozygosity, allelic richness (AR), number of loci exhibiting departures from Hardy-Weinberg Equilibrium (HWE), F_{IS} (a measure of departure from random mating), percent of pairwise tests for linkage disequilibrium yielding significant results (LD), and effective population size (N_e) based on LD are listed for each sample. Samples in which we observed no evidence for any disequilibrium caused by genetic drift due to a finite number of parents (i.e. those with an estimated N_e of infinity) have N_e marked by “-”.

No	Description	H_e	H_o	AR	HWE	F_{IS}	LD	N_e
1	Eagle Creek NFHa 2001	0.84	0.82	10.37	1	0.02	5.5	622 (217 - Infinite)
2	Eagle Creek NFHa 2010	0.84	0.85	10.38	3	0.00	21.8	243 (145 - 597)
3	Eagle Creek NFHa 2011	0.85	0.83	11.57	6	0.03	72.7	90 (73 - 115)
4	Eagle Creek NFHj 2010	0.85	0.84	9.96	3	0.02	29.1	161 (96 - 383)
5	Eagle Creek NFHj 2012	0.83	0.81	10.91	2	0.03	45.5	69 (55 - 91)
6	Big 2002	0.86	0.86	10.82	3	0.00	30.9	95 (66 - 159)
7	Bonneville 2002	0.84	0.84	10.69	1	0.00	7.3	1305 (233 - Infinite)
8	Clackamas-Early 1998	0.87	0.84	10.66	1	0.04	0.0	-
9	Clackamas-Early 2010	0.85	0.83	9.19	1	0.03	21.8	194 (123 - 403)
10	Clackamas-Early 2011	0.86	0.83	8.89	2	0.03	29.1	123 (89 - 185)
11	Clackamas-Late 1998	0.84	0.83	11.00	0	0.01	5.5	-
12	Clackamas-Late 2010	0.83	0.81	10.74	1	0.02	5.5	142 (85 - 343)
13	Clackamas-Late 2011	0.81	0.80	9.29	3	0.01	38.2	72 (50 - 118)
14	Clear 2007	0.84	0.82	10.77	2	0.03	30.9	45 (33 - 66)
15	Clear 2008	0.85	0.83	11.20	1	0.03	7.3	146 (72 - 1254)
16	Clear 2010	0.84	0.82	11.11	2	0.02	10.9	132 (81 - 279)
17	Clear 2011	0.86	0.87	11.06	2	-0.01	7.3	98 (53 - 368)
18	Cowlitz 2002	0.86	0.85	10.17	0	0.01	9.1	1260 (221 - Infinite)
19	Cowlitz 2003	0.84	0.84	10.99	5	0.01	3.6	336 (104 - Infinite)
20	Deep 2007	0.86	0.79	10.20	2	0.07	5.5	187 (95 - 1371)
21	Deep 2008	0.86	0.83	10.77	1	0.04	10.9	240 (129 - 1119)
22	Eagle 2008	0.85	0.85	9.76	1	0.00	12.7	127 (85 - 229)
23	Eagle 2010	0.85	0.83	10.29	3	0.03	9.1	562 (206 - Infinite)
24	Eagle 2011	0.82	0.80	10.62	3	0.03	49.1	55 (44 - 72)
25	Elochoman-Early 2003	0.84	0.84	10.18	1	-0.01	1.8	134 (82 - 321)
26	Elochoman-Late 2003	0.83	0.84	10.34	1	-0.01	5.5	101 (54 - 376)
27	Fallert 2003	0.85	0.83	10.66	2	0.02	7.3	117 (73 - 261)
28	Fallert 2003	0.87	0.86	10.74	0	0.01	3.6	617 (102 - Infinite)
29	Kalama 2003	0.84	0.83	10.68	2	0.02	1.8	146 (56 - Infinite)
30	Kalama 2003	0.84	0.80	10.88	1	0.05	1.8	61 (32 - 269)
31	Lewis-Early 2003	0.85	0.82	10.71	1	0.03	7.3	198 (74 - Infinite)
32	Lewis-Late 2003	0.84	0.82	9.98	2	0.03	9.1	115 (67 - 317)
33	North Fork Eagle 2010	0.84	0.81	9.16	2	0.04	30.9	108 (77 - 167)
34	North Fork Eagle 2011	0.84	0.79	10.83	4	0.05	45.5	57 (44 - 78)
35	Sandy 2002	0.83	0.85	10.88	1	-0.02	21.8	202 (119 - 539)
36	Toutle 2002	0.83	0.81	10.87	3	0.03	36.4	68 (50 - 97)

Figure 1 – Correspondence Analysis (CA) of allele frequencies observed in samples from Eagle Creek NFH and other lower Columbia River coho salmon populations. Sample numbers are those listed in Table 3. Axis 1 and 2 accounted for 11.4%, and 10.2% of the variance, respectively.

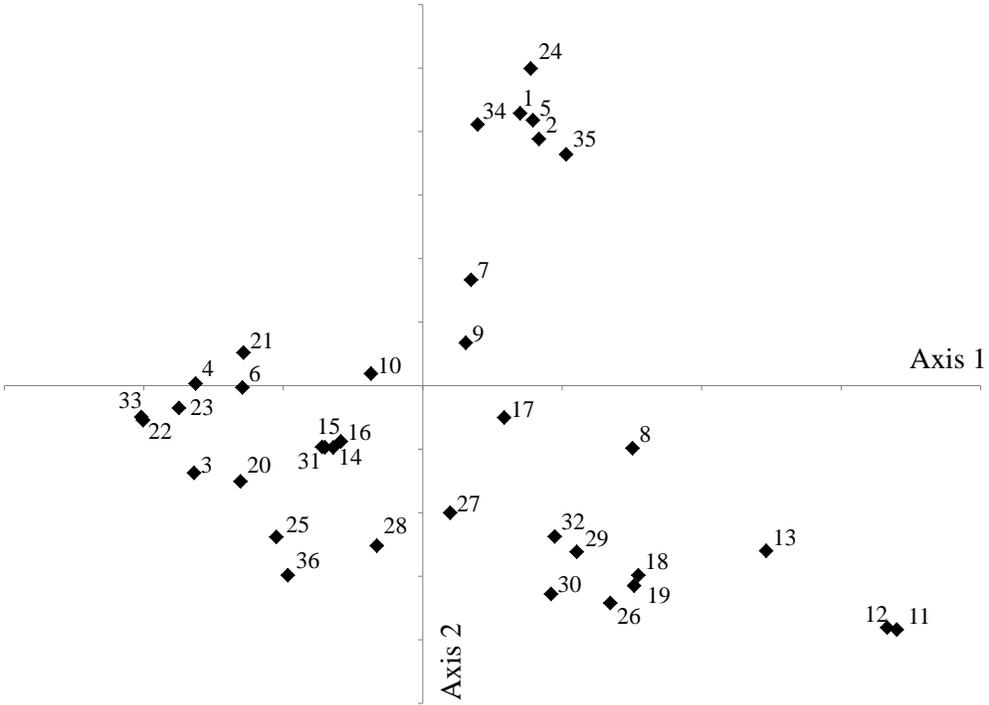
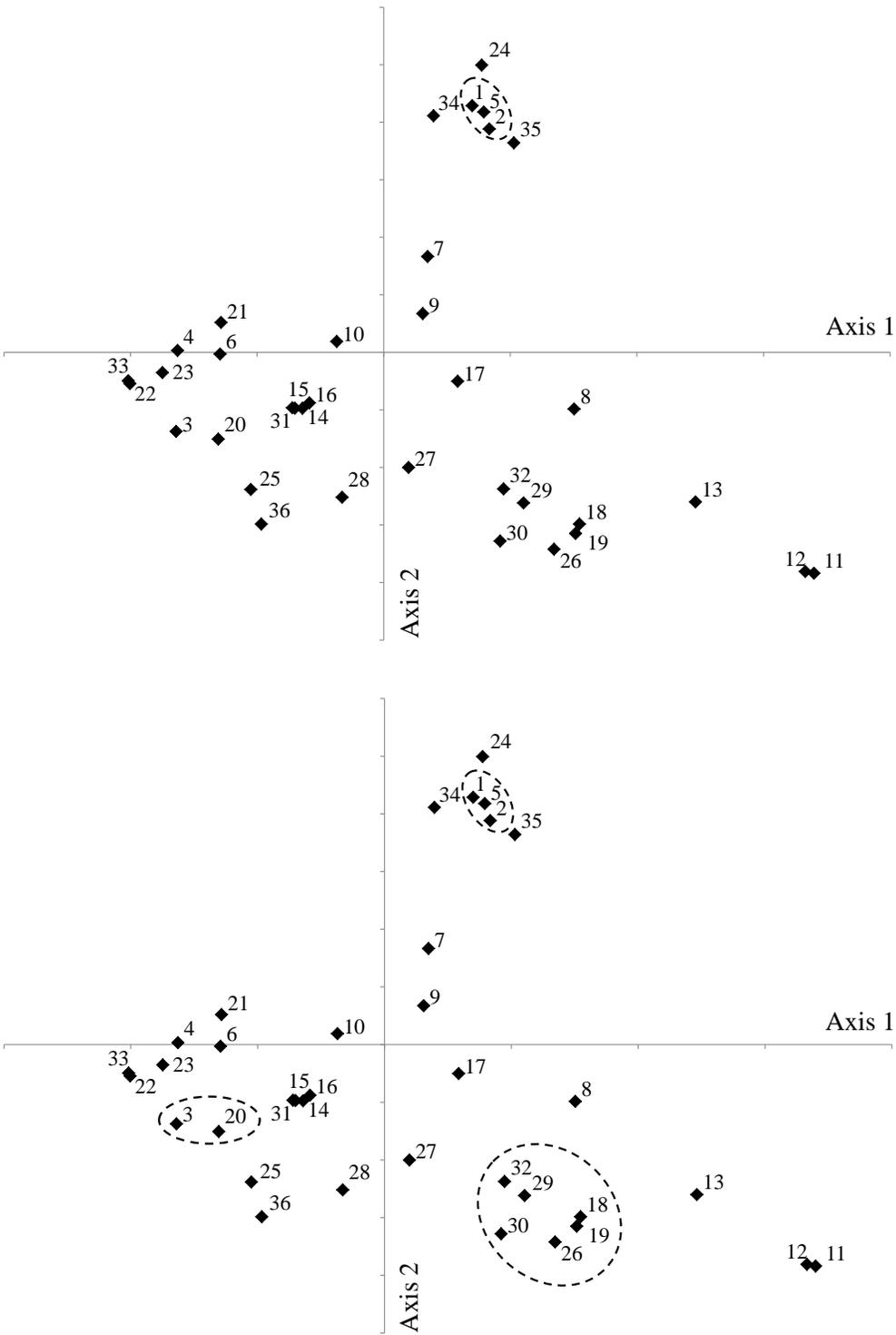


Figure 2 - Statistical tests of divergence among samples from Eagle Creek NFH and other lower Columbia River coho salmon populations. Sample numbers are those listed in Table 3. Dashed lines indicate groups of samples lacking statistically different allele frequencies (top) and statistically significant F_{ST} values (bottom).



Comments

- The goals of this report series are 1) to summarize available genetic information for NFH broodstocks and make that information available to hatchery managers, and 2) to make sure that data for the NFH broodstocks are available for internal hatchery reviews and HET meetings, as well as to our partners.
- The high levels of LD and departures from HWE, in association with positive F_{IS} values in the Eagle Creek NFH broodstock sample collected in 2011 indicate that the collection may include individuals from multiple populations, related individuals, or individuals from two divergent broodlines. This may suggest a potential problem with the sample, so any interpretation of the results for this sample should be made with caution.
- Genetic diversity (H_e , H_o and AR) observed in the Eagle Creek NFH samples is comparable to that observed in samples from the parental stocks (Sandy River, Toutle River, Big Creek, and Elochoman River), and is also comparable to the diversity observed in samples from natural origin coho salmon stocks within the Clackamas River basin (Clackamas, Clear, Deep, Eagle, and North Fork Eagle).
- Correspondence Analysis reveals a pattern of divergence that is predominantly driven by run type and broodlines. Samples from late run collections cluster in the lower right corner of the plot, and are generally isolated from the early run collections. Among early run type collections, there is a general pattern of samples from the same broodline clustering together. For example, the adult Eagle Creek NFH collection from 2010 not only clusters with the juvenile Eagle Creek NFH collection from 2012 as expected (the juveniles are the progeny of the adults), but both collections cluster with the Eagle Creek NFH collection from 2001, as well as other hatchery and natural origin collections from the same broodline (e.g., Eagle 2011, North Fork Eagle 2011, and Sandy 2002). In some instances, either geographic structure and/or a history of stock transfers among hatcheries may confound the divergence among broodlines.
- Tests for allele frequency heterogeneity and F_{ST} significance indicate that there are significant differences among Eagle Creek NFH samples from different broodlines. Non-significant differences within the same broodline were also observed; however, only one broodline includes multiple collections which may be tested. This precludes the finding of homogeneity within all broodlines.

- Due to the high biological significance of natural origin Clackamas River coho salmon within the Lower Columbia River Coho ESU, the USFWS Columbia Basin Hatchery Review Team (HRT) identified the segregated broodstock at Eagle Creek NFH as a potential genetic risk to natural populations in the Clackamas River basin^{Ref 1}. The current results suggest that the natural origin coho salmon stocks within the lower Clackamas River basin (Clear, Deep, and Eagle) are genetically more similar to the non-native Eagle Creek Hatchery population than they are to the upper Clackamas River populations (Clackamas Early and Clackamas Late), which are thought to represent endemic Clackamas River coho stocks. These results suggest that hatchery introgression is occurring in the lower Clackamas River basin and thus confirm the HRT's concerns of genetic risks associated with operating Eagle Creek NFH with a segregated broodstock program.

Sources cited

1. USFWS Columbia Basin Hatchery Review Team. 2007. Eagle Creek NFH Review (FinalReport). Available:
http://www.fws.gov/pacific/Fisheries/Hatcheryreview/Reports/eaglecreek/EagleCreekNFHReview_27July2007.pdf
2. Age composition is based on a ten-year average (2001-2011) calculated from hatchery spawning records as documented in the ECCOS database, provided by Steve Pastor and Doug Olson, Columbia River Fisheries Program Office.
3. Information regarding the microsatellite markers and the baseline in which they are used may be found in the following article:

Van Doornik, D. M., D. J. Teel, D. R. Kuligowski, C. A. Morgan, and E. Casillas. 2007. Genetic analyses provide insight into the early ocean stock distribution and survival of juvenile coho salmon off the coasts of Washington and Oregon. *North American Journal of Fisheries Management* 27:220-237.

Availability

Genotype data and allele frequencies for NFH stocks are available from Abernathy Fish Technology Center upon request.

Disclaimer

The findings and conclusions in this report are those of the author and do not necessarily represent the views of the U.S. Fish and Wildlife Service.

Appendix 1. Eleven microsatellite markers used to analyze Eagle Creek NFH coho salmon.

<u>Microsatellite markers</u>	
1	Ots213
2	OtsG42
3	Oki23
4	Ots505
5	Ocl8
6	Oki10
7	One13
8	Oki1
9	Ots103
10	P53
11	Ots3

Appendix 2. Genotype call rates (completeness of data).

Description	Collection year	Microsatellite call rate
Eagle Creek NFH	2001	0.995
Eagle Creek NFH	2010	0.961
Eagle Creek NFH	2011	0.985
Eagle Creek NFH	2010	0.949
Eagle Creek NFH	2012	0.946
Big	2002	0.948
Bonneville	2002	0.915
Clackamas-Early	1998	0.922
Clackamas-Early	2010	0.995
Clackamas-Early	2011	0.997
Clackamas-Late	1998	0.926
Clackamas-Late	2010	1.000
Clackamas-Late	2011	0.999
Clear	2007	0.988
Clear	2008	0.998
Clear	2010	0.994
Clear	2011	1.000
Cowlitz	2002	0.945
Cowlitz	2003	0.964
Deep	2007	0.998
Deep	2008	0.998
Eagle	2008	0.999
Eagle	2010	0.985
Eagle	2011	0.996
Elochoman-Early	2003	0.975
Elochoman-Late	2003	0.922
Fallert	2003	0.943
Fallert	2003	0.918
Kalama	2003	0.971
Kalama	2003	0.962
Lewis-Early	2003	0.990
Lewis-Late	2003	0.997
North Fork Eagle	2010	0.924
North Fork Eagle	2011	0.961
Sandy	2002	0.993
Toutle	2002	1.000

Appendix 3. Pairwise F_{ST} values between collections of coho salmon. Sample numbers are those listed in Table 3. Shaded cells indicate non-significant results (pairwise F_{ST} values not >95% of a null distribution in which individuals were permuted among samples).

	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	0.001	0.023	0.018	0.002	0.027	0.010	0.015	0.016	0.020	0.032	0.032	0.038	0.017	0.018	0.016	0.020	0.022
2		0.020	0.016	0.000	0.026	0.011	0.011	0.014	0.018	0.025	0.027	0.034	0.017	0.019	0.016	0.016	0.019
3			0.014	0.024	0.015	0.015	0.011	0.014	0.013	0.032	0.031	0.037	0.014	0.019	0.018	0.020	0.021
4				0.016	0.020	0.021	0.017	0.020	0.021	0.033	0.031	0.036	0.017	0.015	0.010	0.020	0.023
5					0.030	0.016	0.016	0.017	0.022	0.031	0.032	0.037	0.020	0.019	0.015	0.019	0.023
6						0.016	0.018	0.023	0.019	0.033	0.041	0.044	0.020	0.027	0.024	0.022	0.025
7							0.007	0.013	0.014	0.027	0.028	0.042	0.012	0.022	0.018	0.019	0.018
8								0.004	0.004	0.011	0.018	0.033	0.011	0.018	0.015	0.011	0.011
9									0.005	0.032	0.029	0.038	0.013	0.024	0.018	0.021	0.017
10										0.032	0.037	0.041	0.010	0.022	0.021	0.025	0.020
11											0.011	0.025	0.023	0.022	0.026	0.017	0.020
12												0.022	0.027	0.028	0.023	0.021	0.024
13													0.033	0.031	0.032	0.037	0.033
14														0.013	0.012	0.020	0.020
15															0.006	0.020	0.026
16																0.016	0.020
17																	0.013

-continued-

Appendix 4. Glossary

Allele – A unique genetic character state. Each locus has two alleles.

Allelic richness – The number of alleles observed in a sample of individuals, corrected for unequal sample sizes by rarefaction.

Effective population size (N_e) – The number of individuals in a model population which would lose genetic variation at the same rate as an observed population. Deviations from model behavior in real populations (e.g. unequal sex ratios, some individuals reproducing more than others, etc...) tend to make N_e lower than census size (N).

F_{IS} – Correlation of alleles in an individual relative to the subpopulation in which it occurs. Commonly used as a measure of departure from random mating within a subpopulation.

F_{ST} – Correlation of alleles within the same subpopulation relative to the entire population. Commonly used as a measure of divergence between subpopulations.

Gene flow – Movement of genetic material from one population to another. Implies both physical movement and successful integration into the recipient population.

Genetic Drift – Process of genetic divergence between populations based on random sampling of alleles each generation.

Heterozygosity – Proportion of individuals in a population that are heterozygotes (i.e. do not have two identical alleles at a locus).

Hardy-Weinberg Equilibrium (HWE) – Genotype ratios expected under a random mating model.

Linkage Disequilibrium (LD) – A measure of departure from independence of alleles in a pair of loci.

Locus – A physical location on the DNA of an organism. The term “locus” is often used synonymously with “marker” or with any type of marker (e.g., “SNP” or “microsatellite”).